

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/550,951
Source: IFWP
Date Processed by STIC: 07/27/2006

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IFWP

RAW SEQUENCE LISTING

DATE: 07/27/2006

PATENT APPLICATION: US/10/550,951

TIME: 12:05:14

Input Set : A:\SAWA3005 Sequence Listing.ST25.txt

Output Set: N:\CRF4\07272006\J550951.raw

Said

3 <110> APPLICANT: Sawadaishi, Kazuyuki

5 <120> TITLE OF INVENTION: Recombinant Antibody Recognizing Dioxin and Gene Encoding

6 Antibody

8 <130> FILE REFERENCE: SAWA3005/ESS

10 <140> CURRENT APPLICATION NUMBER: 10/550,951

11 <141> CURRENT FILING DATE: 2005-09-28

13 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/004355

14 <151> PRIOR FILING DATE: 2004-03-26

16 <150> PRIOR APPLICATION NUMBER: JP 2003-091663

17 <151> PRIOR FILING DATE: 2003-03-28

19 <160> NUMBER OF SEQ ID NOS: 67

21 <170> SOFTWARE: PatentIn version 3.3

23 <210> SEQ ID NO: 1

24 <211> LENGTH: 342

25 <212> TYPE: DNA

26 <213> ORGANISM: Unknown

28 <220> FEATURE:

29 <223> OTHER INFORMATION: DNA encoding polypeptide of H-chain variable region of

monoclonal

30 antibody Dx 3860

33 <220> FEATURE:

34 <221> NAME/KEY: exon

35 <222> LOCATION: (1)..(342)

37 <400> SEQUENCE: 1

38	gaa gtg aag ctg gtg gag tct ggg gga ggc tta gtg aag cct gga ggg	48
39	Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly	
40	1 5 10 15	
42	tcc ctg aaa ctc tcc tgt gca gcc tct gga ttc act ttc agt tcc tat	96
43	Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr	
44	20 25 30	
46	gcc atg tct tgg gtt cgc cag act cca gag aag agg ctg gag tgg gtc	144
47	Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val	
48	35 40 45	
50	gca tcc ttt agt aat ggt ggt atc acc tac tat cca gac agt gtg aag	192
51	Ala Ser Phe Ser Asn Gly Gly Ile Thr Tyr Tyr Pro Asp Ser Val Lys	
52	50 55 60	
54	ggc cga ttc acc atc tcc aga gat aat gcc agg aac atc ctg tac ctg	240
55	Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu	
56	65 70 75 80	
58	caa atg acc agt ctg agg tct gag gac acg gcc att tat tac tgt gca	288
59	Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Ala	
60	85 90 95	
62	aga ggc tat ggt cct gct tac tgg ggc caa ggg act ctg gtc act gtc	336

CP9-7)

. 63 Arg Gly Tyr Gly Pro Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val

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64          100          105          110
66 tct gca                                     342
67 Ser Ala
71 <210> SEQ ID NO: 2
72 <211> LENGTH: 330
73 <212> TYPE: DNA
74 <213> ORGANISM: Unknown
76 <220> FEATURE:
77 <223> OTHER INFORMATION: DNA encoding polypeptide of L-chain variable region of
monoclonal
78      antibody Dx 3860
81 <220> FEATURE:
82 <221> NAME/KEY: exon
83 <222> LOCATION: (1)..(330)
85 <400> SEQUENCE: 2
86 cag gct gtt gtg act cag gaa tct gca ctc acc aca tca cct ggt gaa      48
87 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
88 1          5          10          15
90 aca gtc aca ctc act tgt cgc tca agt act ggg gct gtt aca act ctt      96
91 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Leu
92          20          25          30
94 aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggt      144
95 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
96          35          40          45
98 cta ata ggt aat acc aac aac cga gct cca ggt gtt cct gcc aga ttc      192
99 Leu Ile Gly Asn Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
100          50          55          60
102 tca ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca      240
103 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
104 65          70          75          80
106 cag act gag gat gag gca ata tat ttc tgt gct cta tgg tac agc aac      288
107 Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
108          85          90          95
110 cat ttg gtg ttc ggt gga gga acc aaa ctg act gtc cta ggc      330
111 His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
112          100          105          110
115 <210> SEQ ID NO: 3
116 <211> LENGTH: 354
117 <212> TYPE: DNA
118 <213> ORGANISM: Unknown
120 <220> FEATURE:
121 <223> OTHER INFORMATION: DNA encoding polypeptide of H-chain variable region of
monoclonal
122      antibody Dx 3150
125 <220> FEATURE:
126 <221> NAME/KEY: exon
127 <222> LOCATION: (1)..(354)
129 <400> SEQUENCE: 3
130 gat gta cag ctt cag gag tca gga cct ggc ctc gtg aaa cct tct cag      48
131 Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
132 1          5          10          15

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134 tct ctg tct ctc acc tgt tct gtc act ggc tac tcc atc acc agt ggc      96
135 Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
136          20          25          30
138 ttt tac tgg aac tgg atc cgg cag ttt cca gga aac aaa ctg gaa tgg      144
139 Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
140          35          40          45
142 atg ggc tac ata agc tac gac ggt tac aat aat tac aac cca ttt ctc      192
143 Met Gly Tyr Ile Ser Tyr Asp Gly Tyr Asn Asn Tyr Asn Pro Phe Leu
144          50          55          60
146 aaa aat cga gtg tcc atc act cgt gac aca tct gag aac cag ttt ttc      240
147 Lys Asn Arg Val Ser Ile Thr Arg Asp Thr Ser Glu Asn Gln Phe Phe
148 65          70          75          80
150 ctg aag ttg cat tct gtg act act gag gac aca gct aca tat tac tgt      288
151 Leu Lys Leu His Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
152          85          90          95
154 gta agt tac ggt agt cgg agg gga gtt acc tac tgg ggc caa ggc acc      336
155 Val Ser Tyr Gly Ser Arg Arg Gly Val Thr Tyr Trp Gly Gln Gly Thr
156          100          105          110
158 act ctc aca gtc tcc tca      354
159 Thr Leu Thr Val Ser Ser
160          115
163 <210> SEQ ID NO: 4
164 <211> LENGTH: 330
165 <212> TYPE: DNA
166 <213> ORGANISM: Unknown
168 <220> FEATURE:
169 <223> OTHER INFORMATION: DNA encoding polypeptide of L-chain variable region of
monoclonal
170          antibody Dx 3150
173 <220> FEATURE:
174 <221> NAME/KEY: exon
175 <222> LOCATION: (1)..(330)
177 <400> SEQUENCE: 4
178 cag gct gtt gtg act cag gaa tct gca ctc acc aca tca cct ggt gaa      48
179 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
180 1          5          10          15
182 aca gtc aca ctc act tgt cgc tca agt act ggg gct gtt aca act agt      96
183 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
184          20          25          30
186 aac tat gcc aac tgg gtc caa gaa aaa cca gat cat tta ttc act ggt      144
187 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
188          35          40          45
190 cta ata ggt aat acc aac aac cga gct cca ggt gtt cct gcc aga ttc      192
191 Leu Ile Gly Asn Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
192          50          55          60
194 tct ggc tcc ctg att gga gac aag gct gcc ctc acc atc aca ggg gca      240
195 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
196 65          70          75          80
198 cag act gag gat gag gcg ata tat ttc tgt gct ctt tgg tac aac acc      288
199 Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Asn Thr

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200          85          90          95          330
202 cat ttg gtg ttc ggt gga gga acc aga ctg act gtc cta ggc
203 His Leu Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
204          100          105          110
207 <210> SEQ ID NO: 5
208 <211> LENGTH: 114
209 <212> TYPE: PRT
210 <213> ORGANISM: Unknown
212 <220> FEATURE:
213 <223> OTHER INFORMATION: Polypeptide of H-chain variable region of monoclonal
antibody Dx
214          3860
216 <400> SEQUENCE: 5
218 Glu Val Lys Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
219 1          5          10          15
222 Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
223          20          25          30
226 Ala Met Ser Trp Val Arg Gln Thr Pro Glu Lys Arg Leu Glu Trp Val
227          35          40          45
230 Ala Ser Phe Ser Asn Gly Gly Ile Thr Tyr Tyr Pro Asp Ser Val Lys
231          50          55          60
234 Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Arg Asn Ile Leu Tyr Leu
235 65          70          75          80
238 Gln Met Thr Ser Leu Arg Ser Glu Asp Thr Ala Ile Tyr Tyr Cys Ala
239          85          90          95
242 Arg Gly Tyr Gly Pro Ala Tyr Trp Gly Gln Gly Thr Leu Val Thr Val
243          100          105          110
246 Ser Ala
250 <210> SEQ ID NO: 6
251 <211> LENGTH: 110
252 <212> TYPE: PRT
253 <213> ORGANISM: Unknown
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Polypeptide of L-chain variable region of monoclonal
antibody Dx
257          3860
259 <400> SEQUENCE: 6
261 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
262 1          5          10          15
265 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Leu
266          20          25          30
269 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
270          35          40          45
273 Leu Ile Gly Asn Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
274          50          55          60
277 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
278 65          70          75          80
281 Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Ser Asn
282          85          90          95
285 His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly
286          100          105          110

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Input Set : A:\SAWA3005 Sequence Listing.ST25.txt

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289 <210> SEQ ID NO: 7
290 <211> LENGTH: 118
291 <212> TYPE: PRT
292 <213> ORGANISM: Unknown
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Polypeptide of H-chain variable region of monoclonal
antibody Dx
296         3150
298 <400> SEQUENCE: 7
300 Asp Val Gln Leu Gln Glu Ser Gly Pro Gly Leu Val Lys Pro Ser Gln
301 1         5         10         15
304 Ser Leu Ser Leu Thr Cys Ser Val Thr Gly Tyr Ser Ile Thr Ser Gly
305         20         25         30
308 Phe Tyr Trp Asn Trp Ile Arg Gln Phe Pro Gly Asn Lys Leu Glu Trp
309         35         40         45
312 Met Gly Tyr Ile Ser Tyr Asp Gly Tyr Asn Asn Tyr Asn Pro Phe Leu
313         50         55         60
316 Lys Asn Arg Val Ser Ile Thr Arg Asp Thr Ser Glu Asn Gln Phe Phe
317 65         70         75         80
320 Leu Lys Leu His Ser Val Thr Thr Glu Asp Thr Ala Thr Tyr Tyr Cys
321         85         90         95
324 Val Ser Tyr Gly Ser Arg Arg Gly Val Thr Tyr Trp Gly Gln Gly Thr
325         100        105        110
328 Thr Leu Thr Val Ser Ser
329         115
332 <210> SEQ ID NO: 8
333 <211> LENGTH: 110
334 <212> TYPE: PRT
335 <213> ORGANISM: Unknown
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Polypeptide of L-chain variable region of monoclonal
antibody Dx
339         3150
341 <400> SEQUENCE: 8
343 Gln Ala Val Val Thr Gln Glu Ser Ala Leu Thr Thr Ser Pro Gly Glu
344 1         5         10         15
347 Thr Val Thr Leu Thr Cys Arg Ser Ser Thr Gly Ala Val Thr Thr Ser
348         20         25         30
351 Asn Tyr Ala Asn Trp Val Gln Glu Lys Pro Asp His Leu Phe Thr Gly
352         35         40         45
355 Leu Ile Gly Asn Thr Asn Asn Arg Ala Pro Gly Val Pro Ala Arg Phe
356         50         55         60
359 Ser Gly Ser Leu Ile Gly Asp Lys Ala Ala Leu Thr Ile Thr Gly Ala
360 65         70         75         80
363 Gln Thr Glu Asp Glu Ala Ile Tyr Phe Cys Ala Leu Trp Tyr Asn Thr
364         85         90         95
367 His Leu Val Phe Gly Gly Gly Thr Arg Leu Thr Val Leu Gly
368         100        105        110
371 <210> SEQ ID NO: 9
372 <211> LENGTH: 8
373 <212> TYPE: PRT

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:23; N Pos. 30

Seq#:25; N Pos. 24

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42

Seq#:43,44,45,46,47,48,49,50,51,52,53,54,55

VERIFICATION SUMMARY

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L:584 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23 after pos.:0

L:614 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25 after pos.:0